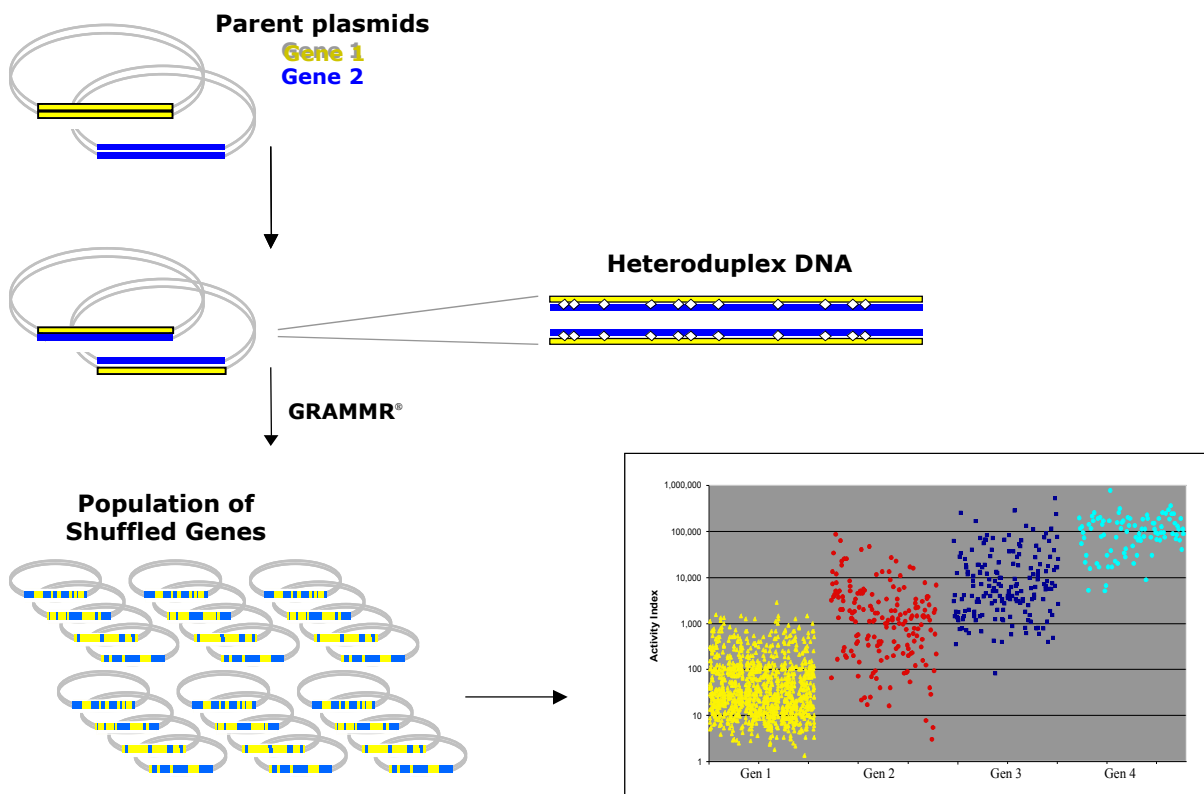


GRAMMR[®] GENE SHUFFLING PLATFORM

Genetic ReAssortment by MisMatch Resolution

- Efficiently shuffles distantly related genes** – ~60-99 percent identity
- No cloning or PCR required** – works in context of existing plasmids/cosmids
- Not size dependent** – works on large genes & can shuffle multiple genes simultaneously
- Low % of parent clones** – minimal parental carryover for increased screening efficiency
- Minimizes genetic founder effects** – maximizes diversity in progeny population
- Minimizes mutations and rearrangements** – high percentage of intact genes



Fast	<ul style="list-style-type: none"> • Generates diverse libraries of shuffled progeny clones in a day
Flexible	<ul style="list-style-type: none"> • Compatible with a wide variety of cell types and vector systems
High-Quality Libraries	<ul style="list-style-type: none"> • High crossover frequency and resolution • Uniform distribution of crossovers results in fewer hotspots • Minimal gene rearrangement
Cost Effective	<ul style="list-style-type: none"> • Custom workflows to fit your needs: shuffling, expression, screening
Informatics	<ul style="list-style-type: none"> • Customized bioinformatic package for analysis of shuffled libraries
IP	<ul style="list-style-type: none"> • Six issued US Patents & various issued foreign patents